GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 9, 2005, 18:15:28 ; Search time 497 Seconds
(without alignments)
366.068 Million cell updates/sec

Title: US-09-937-057-9
Perfect score: 22
Sequence: 1 tgactgtgaacgttatagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 11332426

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
24: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
25: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
27: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
28: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	22	9	US-09-967-881-9	Sequence 9, Appli
2	20.4	92.7	22	9	US-09-791-500-5	Sequence 5, Appli
3	20.4	92.7	22	9	US-09-791-500-6	Sequence 6, Appli
4	20.4	92.7	22	9	US-09-770-943-2	Sequence 2, Appli
5	20.4	92.7	22	10	US-09-848-986-10	Sequence 10, Appl
6	20.4	92.7	22	10	US-09-848-986-11	Sequence 11, Appl
7	20.4	92.7	22	16	US-10-233-121A-10	Sequence 10, Appl
8	20.4	92.7	22	16	US-10-219-143-5	Sequence 5, Appli
9	20.4	92.7	22	16	US-10-219-143-6	Sequence 6, Appli
10	20.4	92.7	22	17	US-10-412-151-5	Sequence 5, Appli
11	20.4	92.7	22	17	US-10-412-151-6	Sequence 6, Appli
12	19.4	88.2	22	16	US-10-233-121A-11	Sequence 11, Appl
13	18.8	85.5	22	9	US-09-802-686-1	Sequence 1, Appli
14	18.8	85.5	22	9	US-09-802-686-4	Sequence 4, Appli
15	18.8	85.5	22	9	US-09-802-686-9	Sequence 9, Appli
16	18.8	85.5	22	9	US-09-802-685-1	Sequence 1, Appli
17	18.8	85.5	22	9	US-09-802-685-4	Sequence 4, Appli
18	18.8	85.5	22	9	US-09-802-685-9	Sequence 9, Appli
19	18.8	85.5	22	9	US-09-802-685-12	Sequence 12, Appl
20	18.8	85.5	22	9	US-09-791-500-1	Sequence 1, Appli
21	18.8	85.5	22	9	US-09-791-500-3	Sequence 3, Appli
22	18.8	85.5	22	9	US-09-791-500-8	Sequence 8, Appli
23	18.8	85.5	22	9	US-09-802-376-1	Sequence 1, Appli
24	18.8	85.5	22	9	US-09-802-376-4	Sequence 4, Appli
25	18.8	85.5	22	9	US-09-802-376-9	Sequence 9, Appli
26	18.8	85.5	22	9	US-09-802-376-10	Sequence 10, Appl
27	18.8	85.5	22	9	US-09-774-403A-1	Sequence 1, Appli
28	18.8	85.5	22	9	US-09-774-403A-3	Sequence 3, Appli
29	18.8	85.5	22	9	US-09-770-943-1	Sequence 1, Appli
30	18.8	85.5	22	9	US-09-770-943-3	Sequence 3, Appli
31	18.8	85.5	22	9	US-09-770-943-10	Sequence 10, Appl
32	18.8	85.5	22	9	US-09-802-370-1	Sequence 1, Appli
33	18.8	85.5	22	9	US-09-802-370-4	Sequence 4, Appli
34	18.8	85.5	22	9	US-09-802-445-1	Sequence 1, Appli
35	18.8	85.5	22	9	US-09-802-445-4	Sequence 4, Appli
36	18.8	85.5	22	9	US-09-820-484-1	Sequence 1, Appli
37	18.8	85.5	22	9	US-09-820-484-3	Sequence 3, Appli
38	18.8	85.5	22	9	US-09-820-484-7	Sequence 7, Appli
39	18.8	85.5	22	9	US-09-828-505-1	Sequence 1, Appli
40	18.8	85.5	22	9	US-09-828-505-4	Sequence 4, Appli
41	18.8	85.5	22	9	US-09-967-881-1	Sequence 1, Appli
42	18.8	85.5	22	9	US-09-967-881-2	Sequence 2, Appli
43	18.8	85.5	22	9	US-09-967-881-3	Sequence 3, Appli
44	18.8	85.5	22	10	US-09-927-422A-1	Sequence 1, Appli
45	18.8	85.5	22	10	US-09-927-422A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-967-881-9
; Sequence 9, Application US/09967881
; Publication No. US20020192184A1
; GENERAL INFORMATION:
; APPLICANT: Assistance Publique - Hopitaux de Paris
; APPLICANT: Institut National de la Sante et de la Recherche M
; APPLICANT: Carpentier, Antoine
; TITLE OF INVENTION: Use of Stabilised Oligonucleotides for Preparing A Medicament wit
; TITLE OF INVENTION: Antitumor Activity
; FILE REFERENCE: 267/246 US
; CURRENT APPLICATION NUMBER: US/09/967,881
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligodeoxynucleotide
US-09-967-881-9

Query Match 100.0%; Score 22; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22

```
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTATAGATGA 22


RESULT 2
US-09-791-500-5
; Sequence 5, Application US/09791500
; Patent No. US20020042387A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: 6510-202US1
;  CURRENT APPLICATION NUMBER: US/09/791,500
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-5

  Query Match             92.7%;  Score 20.4;  DB 9;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 9.9;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 3
US-09-791-500-6
; Sequence 6, Application US/09791500
; Patent No. US20020042387A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: 6510-202US1
;  CURRENT APPLICATION NUMBER: US/09/791,500
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-6

  Query Match             92.7%;  Score 20.4;  DB 9;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 9.9;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 4
US-09-770-943-2
; Sequence 2, Application US/09770943
; Publication No. US20020086839A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Roman, Mark
;  TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
;  TITLE OF INVENTION:  Sequence Activity
;  FILE REFERENCE: 6510-173US1
;  CURRENT APPLICATION NUMBER: US/09/770,943
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: 09/092,314
;  PRIOR FILING DATE: 1998-06-05
;  PRIOR APPLICATION NUMBER: 60/048,794
;  PRIOR FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-770-943-2

  Query Match             92.7%;  Score 20.4;  DB 9;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 9.9;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 5
US-09-848-986-10
; Sequence 10, Application US/09848986
; Publication No. US20030176373A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Lois, Augusto F.
;  APPLICANT:  Takabayashi, Kenji
;  TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
;  TITLE OF INVENTION:  Methods of Use Thereof
;  FILE REFERENCE: 06510168US1
;  CURRENT APPLICATION NUMBER: US/09/848,986
;  CURRENT FILING DATE:  2001-05-03
;  PRIOR APPLICATION NUMBER: us 60/262321
;  PRIOR FILING DATE: 2001-01-17
;  PRIOR APPLICATION NUMBER: us 60/202,274
;  PRIOR FILING DATE: 2000-05-05
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: ISS-ODN
US-09-848-986-10

  Query Match             92.7%;  Score 20.4;  DB 10;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 9.9;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 6
US-09-848-986-11
; Sequence 11, Application US/09848986
; Publication No. US20030176373A1
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Lois, Augusto F.
;  APPLICANT:  Takabayashi, Kenji
;  TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
```

; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 06510168US1
; CURRENT APPLICATION NUMBER: US/09/848,986
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: us 60/262321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: us 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: methylated ISS-ODN
; NAME/KEY: modified_base
; LOCATION: (11)...(11)
; OTHER INFORMATION: m5c
US-09-848-986-11

Query Match 92.7%; Score 20.4; DB 10; Length 22;
Best Local Similarity 95.5%; Pred. No. 9.9;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||||| ||||||
Db 1 TGACTGTGAACGTTAGAGATGA 22

RESULT 7
US-10-233-121A-10
; Sequence 10, Application US/10233121A
; Publication No. US20030125284A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, EYAL
; APPLICANT: LOIS, AUGUSTO
; APPLICANT: TAKABAYASHI, KENJI
; TITLE OF INVENTION: AGENTS THAT MODULATE DNA-PK ACTIVITY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: UCAL-168DIV
; CURRENT APPLICATION NUMBER: US/10/233,121A
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 09/848,986
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/202,274
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/262,321
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphodiester or phosphorothioate oligonucleotide
US-10-233-121A-10

Query Match 92.7%; Score 20.4; DB 16; Length 22;
Best Local Similarity 95.5%; Pred. No. 9.9;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||||| ||||||
Db 1 TGACTGTGAACGTTAGAGATGA 22

RESULT 8
US-10-219-143-5
; Sequence 5, Application US/10219143
; Publication No. US20030130217A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202US1
; CURRENT APPLICATION NUMBER: US/10/219,143
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/791,500
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-10-219-143-5

Query Match 92.7%; Score 20.4; DB 16; Length 22;
Best Local Similarity 95.5%; Pred. No. 9.9;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||||| ||||||
Db 1 TGACTGTGAACGTTAGAGATGA 22

RESULT 9
US-10-219-143-6
; Sequence 6, Application US/10219143
; Publication No. US20030130217A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202US1
; CURRENT APPLICATION NUMBER: US/10/219,143
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/791,500
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-10-219-143-6

Query Match 92.7%; Score 20.4; DB 16; Length 22;
Best Local Similarity 95.5%; Pred. No. 9.9;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||||| ||||||
Db 1 TGACTGTGAACGTTAGAGATGA 22

RESULT 10
US-10-412-151-5
; Sequence 5, Application US/10412151
; Publication No. US20030176389A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: UCAL-202CON
; CURRENT APPLICATION NUMBER: US/10/412,151
; CURRENT FILING DATE: 2003-04-11

; PRIOR APPLICATION NUMBER: 09/791,500
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,256
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-10-412-151-5

Query Match 92.7%; Score 20.4; DB 17; Length 22;
Best Local Similarity 95.5%; Pred. No. 9.9;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||||| ||||||
Db 1 TGACTGTGAACGTTAGAGATGA 22

RESULT 11
US-10-412-151-6
; Sequence 6, Application US/10412151
; Publication No. US20030176389A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: UCAL-202CON
; CURRENT APPLICATION NUMBER: US/10/412,151
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 09/791,500
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/184,256
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-10-412-151-6

Query Match 92.7%; Score 20.4; DB 17; Length 22;
Best Local Similarity 95.5%; Pred. No. 9.9;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||||| ||||||
Db 1 TGACTGTGAACGTTAGAGATGA 22

RESULT 12
US-10-233-121A-11
; Sequence 11, Application US/10233121A
; Publication No. US20030125284A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, EYAL
; APPLICANT: LOIS, AUGUSTO
; APPLICANT: TAKABAYASHI, KENJI
; TITLE OF INVENTION: AGENTS THAT MODULATE DNA-PK ACTIVITY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: UCAL-168DIV
; CURRENT APPLICATION NUMBER: US/10/233,121A
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 09/848,986
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/202,274
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/262,321
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n = 5-methylcytidine-phosphodiester or
; OTHER INFORMATION: 5-methylcytidine-phosphorothioate
US-10-233-121A-11

Query Match 88.2%; Score 19.4; DB 16; Length 22;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
|||||||||| |||| ||||||
Db 1 TGACTGTGAANGTTAGAGATGA 22

RESULT 13
US-09-802-686-1
; Sequence 1, Application US/09802686
; Patent No. US20010046967A1
; GENERAL INFORMATION:
; APPLICANT: Dynavax Technologies Corporation
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING
; TITLE OF INVENTION: RESPIRATORY VIRAL INFECTION USING IMMUNOMODULATORY
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES
; FILE REFERENCE: 377882000900
; CURRENT APPLICATION NUMBER: US/09/802,686
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,583
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-686-1

Query Match 85.5%; Score 18.8; DB 9; Length 22;
Best Local Similarity 90.9%; Pred. No. 57;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||||| ||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 14
US-09-802-686-4
; Sequence 4, Application US/09802686
; Patent No. US20010046967A1
; GENERAL INFORMATION:
; APPLICANT: Dynavax Technologies Corporation
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING
; TITLE OF INVENTION: RESPIRATORY VIRAL INFECTION USING IMMUNOMODULATORY
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES
; FILE REFERENCE: 377882000900
; CURRENT APPLICATION NUMBER: US/09/802,686
; CURRENT FILING DATE: 2001-03-09

```
;  PRIOR APPLICATION NUMBER: 60/188,583
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide containing CG
US-09-802-686-4

  Query Match             85.5%;  Score 18.8;  DB 9;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 57;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||  ||||||
Db          1 TGACTGTGAACGTTCCAGATGA 22


RESULT 15
US-09-802-686-9
; Sequence 9, Application US/09802686
; Patent No. US20010046967A1
; GENERAL INFORMATION:
;  APPLICANT: Dynavax Technologies Corporation
;  APPLICANT:  Van Nest, Gary
;  TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING
;  TITLE OF INVENTION:  RESPIRATORY VIRAL INFECTION USING IMMUNOMODULATORY
;  TITLE OF INVENTION:  POLYNUCLEOTIDE SEQUENCES
;  FILE REFERENCE: 377882000900
;  CURRENT APPLICATION NUMBER: US/09/802,686
;  CURRENT FILING DATE:  2001-03-09
;  PRIOR APPLICATION NUMBER: 60/188,583
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Polynucleotide not containing CG
US-09-802-686-9

  Query Match             85.5%;  Score 18.8;  DB 9;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 57;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||| |||| ||||||
Db          1 TGACTGTGAAGGTTAGAGATGA 22


Search completed: November  9, 2005, 19:28:46
Job time : 504 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 9, 2005, 18:04:54 ; Search time 1762 Seconds
(without alignments)
475.263 Million cell updates/sec

Title: US-09-937-057-9
Perfect score: 22
Sequence: 1 tgactgtgaacgttatagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 675282

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15.6	70.9	81	9	CG620747	CG620747 OST318195
	2	15.6	70.9	86	9	CG548982	CG548982 OST151485
	3	15.6	70.9	90	9	CG546017	CG546017 OST144930
	4	15.6	70.9	91	9	CG554726	CG554726 OST168626
	5	15.6	70.9	97	9	CG631426	CG631426 OST347804
	6	15.6	70.9	98	9	CG610654	CG610654 OST294314
	7	15.6	70.9	100	9	CG496629	CG496629 OST36752
c	8	14.6	66.4	58	1	AI662714	AI662714 va88c01.x
	9	14.6	66.4	58	8	BH908898	BH908898 SALK_0511
c	10	14.4	65.5	70	9	CG546804	CG546804 OST146791
	11	14.4	65.5	80	6	CD384499	CD384499 PTMM09672
	12	14.2	64.5	72	9	CG631425	CG631425 OST347803
	13	14.2	64.5	97	4	BI881470	BI881470 fm93a10.y
c	14	14	63.6	48	8	AZ843479	AZ843479 2M0142C23
	15	14	63.6	63	8	AZ431742	AZ431742 1M0216O18
	16	14	63.6	63	9	CG631431	CG631431 OST347811
c	17	14	63.6	67	8	BH911627	BH911627 SALK_0698
c	18	14	63.6	84	7	CK103587	CK103587 G123P25.5
c	19	14	63.6	86	9	CG640878	CG640878 OST374526
c	20	14	63.6	88	1	AI953694	AI953694 wq47c06.x
c	21	14	63.6	90	9	AG195135	AG195135 Pan trogl
	22	14	63.6	97	6	CD866080	AZO2.102I
c	23	14	63.6	98	1	AA464890	AA464890 aa93d06.r
	24	14	63.6	100	7	CV064730	CV064730 WNEL14d9
	25	13.6	61.8	62	1	AV403764	AV403764 AV403764
	26	13.6	61.8	64	4	BG514647	BG514647 dad63b05.
	27	13.6	61.8	78	9	CG562292	CG562292 OST184609
c	28	13.6	61.8	80	2	BE329424	BE329424 hq37b06.x
	29	13.6	61.8	81	7	CO514377	CO514377 s13dSG84G
c	30	13.6	61.8	82	1	AA573133	AA573133 nj41g02.s
	31	13.6	61.8	92	1	AA462609	AA462609 vg75d04.r
	32	13.6	61.8	92	9	CG578258	CG578258 OST215285
c	33	13.6	61.8	100	1	AI971012	AI971012 wr22g07.x
c	34	13.6	61.8	100	2	AW355356	AW355356 pnf-b.pk0
	35	13.6	61.8	100	7	H16183	H16183 ym21h12.r1
	36	13.4	60.9	51	9	AG199950	AG199950 Pan trogl
	37	13.4	60.9	56	8	BZ664941	BZ664941 SALK_1103
	38	13.4	60.9	82	9	AG198560	AG198560 Pan trogl
	39	13.4	60.9	88	8	AZ783178	AZ783178 2M0024H07
	40	13.2	60.0	40	1	AA779179	AA779179 zj43c07.s
c	41	13.2	60.0	50	1	AI241767	AI241767 qu68c01.x
	42	13.2	60.0	68	9	CC797276	CC797276 SALK_1447
c	43	13.2	60.0	75	9	BX132834	BX132834 Danio rer
	44	13.2	60.0	79	7	CR560685	CR560685 CR560685
	45	13.2	60.0	83	8	BZ765063	BZ765063 SALK_1282

ALIGNMENTS

RESULT 1
CG620747
LOCUS CG620747 81 bp mRNA linear GSS 02-OCT-2003
DEFINITION OST318195 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST318195, mRNA sequence.
ACCESSION CG620747
VERSION CG620747.1 GI:37444596
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 81)
AUTHORS Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.
TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
FEATURES Location/Qualifiers
source 1. .81
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST318195"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

Query Match 70.9%; Score 15.6; DB 9; Length 81;
Best Local Similarity 81.8%; Pred. No. 5.7e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22

```
              |||| | |||||| ||||| ||
Db         30 TGACCGAGAACGTGATAGAGGA 51


RESULT 2
CG548982
LOCUS       CG548982                  86 bp    mRNA    linear   GSS 01-OCT-2003
DEFINITION  OST151485 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST151485,
            mRNA sequence.
ACCESSION   CG548982
VERSION     CG548982.1  GI:37335569
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 86)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .86
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST151485"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             70.9%;  Score 15.6;  DB 9;  Length 86;
  Best Local Similarity   81.8%;  Pred. No. 5.7e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||| | |||||| ||||| ||
Db         35 TGACCGAGAACGTGATAGAGGA 56


RESULT 3
CG546017
LOCUS       CG546017                  90 bp    mRNA    linear   GSS 01-OCT-2003
DEFINITION  OST144930 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST144930,
            mRNA sequence.
ACCESSION   CG546017
VERSION     CG546017.1  GI:37332604
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 90)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .90
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST144930"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             70.9%;  Score 15.6;  DB 9;  Length 90;
  Best Local Similarity   81.8%;  Pred. No. 5.8e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||| | |||||| ||||| ||
Db         39 TGACCGAGAACGTGATAGAGGA 60


RESULT 4
CG554726
LOCUS       CG554726                  91 bp    mRNA    linear   GSS 01-OCT-2003
DEFINITION  OST168626 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST168626,
            mRNA sequence.
ACCESSION   CG554726
VERSION     CG554726.1  GI:37341313
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 91)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .91
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST168626"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
```

```
ORIGIN

  Query Match             70.9%;  Score 15.6;  DB 9;  Length 91;
  Best Local Similarity   81.8%;  Pred. No. 5.8e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||| | |||||| ||||| ||
Db         40 TGACCGAGAACGTGATAGAGGA 61


RESULT 5
CG631426
LOCUS       CG631426                 97 bp    mRNA    linear   GSS 02-OCT-2003
DEFINITION  OST347804 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST347804,
            mRNA sequence.
ACCESSION   CG631426
VERSION     CG631426.1  GI:37455275
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 97)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .97
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST347804"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             70.9%;  Score 15.6;  DB 9;  Length 97;
  Best Local Similarity   81.8%;  Pred. No. 5.8e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||| | |||||| ||||| ||
Db         46 TGACCGAGAACGTGATAGAGGA 67


RESULT 6
CG610654
LOCUS       CG610654                 98 bp    mRNA    linear   GSS 02-OCT-2003
DEFINITION  OST294314 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST294314,
            mRNA sequence.
ACCESSION   CG610654
VERSION     CG610654.1  GI:37434503
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 98)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .98
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST294314"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             70.9%;  Score 15.6;  DB 9;  Length 98;
  Best Local Similarity   81.8%;  Pred. No. 5.8e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||| | |||||| ||||| ||
Db         47 TGACCGAGAACGTGATAGAGGA 68


RESULT 7
CG496629
LOCUS       CG496629                100 bp    mRNA    linear   GSS 01-OCT-2003
DEFINITION  OST36752 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST36752,
            mRNA sequence.
ACCESSION   CG496629
VERSION     CG496629.1  GI:37265188
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 100)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .100
```

```
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST36752"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             70.9%;  Score 15.6;  DB 9;  Length 100;
  Best Local Similarity   81.8%;  Pred. No. 5.9e+03;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||| | |||||| ||||| ||
Db         49 TGACCGAGAACGTGATAGAGGA 70


RESULT 8
AI662714/c
LOCUS       AI662714                 58 bp    mRNA    linear   EST 10-MAY-1999
DEFINITION  va88c01.x1 Soares mouse 3NME12 5 Mus musculus cDNA clone
            IMAGE:746496 3' similar to TR:O88760 O88760 AF-9 PROTEIN. ;, mRNA
            sequence.
ACCESSION   AI662714
VERSION     AI662714.1  GI:4766297
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 58)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: va88c01.y1
            Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:455480
            This clone was previously sequenced on the 5' end only, this new
            data is from the 3' end
            Possible reversed clone: similarity on wrong strand
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .58
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:746496"
                     /sex="unknown"
                     /tissue_type="fetus"
                     /dev_stage="12.5dpc total fetus"
                     /lab_host="DH10B"
                     /clone_lib="Soares mouse 3NME12 5"
                     /note="Organ: whole fetus; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Not I - oligo(dT) primer
                     [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCTTATTTTTTTTTTTTTTTTT
                     3'],  on total  mouse RNA [provided by Minoru Ko, Wayne
                     State Univ.]; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pT7T3 vector.
                     Library went through one round of normalization, and was
                     constructed by Bento Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match             66.4%;  Score 14.6;  DB 1;  Length 58;
  Best Local Similarity   81.0%;  Pred. No. 1.7e+04;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 GACTGTGAACGTTATAGATGA 22
              || |||| || ||||||| ||
Db         29 GATTGTGGACCTTATAGAGGA 9


RESULT 9
BH908898
LOCUS       BH908898                 58 bp    DNA     linear   GSS 04-SEP-2002
DEFINITION  SALK_051118.17.90.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_051118.17.90.x, genomic
            survey sequence.
ACCESSION   BH908898
VERSION     BH908898.1  GI:22721831
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 58)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated intron of At1g71692.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .58
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_051118.17.90.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match             66.4%;  Score 14.6;  DB 8;  Length 58;
  Best Local Similarity   81.0%;  Pred. No. 1.7e+04;
  Matches   17;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATG 21
              | ||||| || || |||||||
Db          9 TTACTGTTAAAGTAATAGATG 29


RESULT 10
CG546804/c
LOCUS       CG546804                 70 bp    mRNA    linear   GSS 01-OCT-2003
DEFINITION  OST146791 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST146791,
```

```
            mRNA sequence.
ACCESSION   CG546804
VERSION     CG546804.1  GI:37333391
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .70
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST146791"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             65.5%;  Score 14.4;  DB 9;  Length 70;
  Best Local Similarity   93.8%;  Pred. No. 2.2e+04;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TGAACGTTATAGATGA 22
              |||| ||||||||||
Db         67 TGAAAGTTATAGATGA 52


RESULT 11
CD384499
LOCUS       CD384499                  80 bp    mRNA    linear   EST 31-MAY-2003
DEFINITION  PTMM09672 Phaeodactylum tricornutum Uni-Zap XR Phaeodactylum
            tricornutum cDNA 5', mRNA sequence.
ACCESSION   CD384499
VERSION     CD384499.1  GI:31260113
KEYWORDS    EST.
SOURCE      Phaeodactylum tricornutum
  ORGANISM  Phaeodactylum tricornutum
            Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
            Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
REFERENCE   1  (bases 1 to 80)
  AUTHORS   Scala,S., Carels,N., Falciatore,A., Chiusano,M.L. and Bowler,C.
  TITLE     Genome properties of the diatom Phaeodactylum tricornutum
  JOURNAL   Plant Physiol. 129 (3), 993-1002 (2002)
  MEDLINE   22111123
   PUBMED   12114555
COMMENT     Contact: Bowler C
            Laboratory of Molecular Plant Biology
            Stazione Zoologica 'Anton Dohrn'
            Villa Comunale, I-80121, Napoli, Italy
            Tel: 39 081 583 3268/3211
            Fax: 39 081 764 1355
            Email: chris@alpha.szn.it
            Diatom EST Database(http://avesthagen.sznbowler.com)
            Seq primer: T3 backward
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .80
                     /organism="Phaeodactylum tricornutum"
                     /mol_type="mRNA"
                     /db_xref="taxon:2850"
                     /cell_line="CCMP632"
                     /clone_lib="Phaeodactylum tricornutum Uni-Zap XR"
                     /note="Vector: Uni-Zap XR vector; Site_1: Eco RI; Site_2:
                     Xho I"
ORIGIN

  Query Match             65.5%;  Score 14.4;  DB 6;  Length 80;
  Best Local Similarity   93.8%;  Pred. No. 2.2e+04;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 CTGTGAACGTTATAGA 19
              |||| ||||||||||
Db         47 CTGTTAACGTTATAGA 62


RESULT 12
CG631425
LOCUS       CG631425                  72 bp    mRNA    linear   GSS 02-OCT-2003
DEFINITION  OST347803 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST347803,
            mRNA sequence.
ACCESSION   CG631425
VERSION     CG631425.1  GI:37455274
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 72)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .72
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST347803"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             64.5%;  Score 14.2;  DB 9;  Length 72;
  Best Local Similarity   76.2%;  Pred. No. 2.7e+04;
  Matches   16;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 GACTGTGAACGTTATAGATGA 22
              ||| | |||||| || || ||
Db         29 GACCGAGAACGTGATNGANGA 49
```

```
RESULT 13
BI881470
LOCUS       BI881470                 97 bp    mRNA    linear   EST 16-SEP-2002
DEFINITION  fm93a10.y1 Zebrafish Research Genetics C32 fin Danio rerio cDNA
            clone IMAGE:4468146 5' similar to TR:Q9W725 Q9W725 UNCOUPLING
            PROTEIN 2. ;, mRNA sequence.
ACCESSION   BI881470
VERSION     BI881470.1  GI:16088741
KEYWORDS    EST.
SOURCE      Danio rerio (zebrafish)
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
            Cypriniformes; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 97)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M.,
            Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
            Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
            Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by: Steve
            Johnson. DNA Sequencing by: Washington University Genome Sequencing
            Center NOTE: This clone is available royalty-free through LLNL;
            contact the IMAGE Consortium (info.llnl.gov)for further
            information.
            Trace considered overall poor quality
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .97
                     /organism="Danio rerio"
                     /mol_type="mRNA"
                     /db_xref="taxon:7955"
                     /clone="IMAGE:4468146"
                     /tissue_type="Fin"
                     /lab_host="GeneHogs (HS996, a phage-resistant isolate of
                     DH10B)"
                     /clone_lib="Zebrafish Research Genetics C32 fin"
                     /note="Vector: pT7T3D-Pac with a modified polylinker;
                     Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was prepared
                     from zebrafish(C32) fin, and was then primed with a Not I
                     - oligo(dT) primer. Double-stranded cDNA was ligated to
                     Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector.  Library is non-normalized. Library was
                     constructed by Ning Wu. NOTE: This clone is available
                     royalty-free through LLNL; contact the IMAGE Consortium
                     (info.llnl.gov)for further information"
ORIGIN

  Query Match           64.5%;  Score 14.2;  DB 4;  Length 97;
  Best Local Similarity   84.2%;  Pred. No. 2.9e+04;
  Matches   16;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 ACTGTGAACGTTATAGATG 21
              || |||||||||||  | ||
Db         38 ACCGTGAACGTTATTGGTG 56


RESULT 14
AZ843479/c
LOCUS       AZ843479                 48 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0142C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0142C23 F, genomic survey sequence.
ACCESSION   AZ843479
VERSION     AZ843479.1  GI:13013387
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0142  row: C  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 48.
FEATURES             Location/Qualifiers
     source          1. .48
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0142C23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match           63.6%;  Score 14;  DB 8;  Length 48;
  Best Local Similarity   77.3%;  Pred. No. 3.2e+04;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||| ||  |||| || |
Db         37 TGACTGTGTACTCTATAAATAA 16


RESULT 15
AZ431742
LOCUS       AZ431742                 63 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0216O18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0216O18 R, genomic survey sequence.
```

```
ACCESSION   AZ431742
VERSION     AZ431742.1  GI:10555755
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 63)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0216  row: O  column: 18
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 63.
FEATURES             Location/Qualifiers
     source          1. .63
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0216O18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             63.6%;  Score 14;  DB 8;  Length 63;
  Best Local Similarity   77.3%;  Pred. No. 3.4e+04;
  Matches   17;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||| |||||| ||| | ||||
Db         36 TGAATGTGAATGTTTGAAATGA 57


Search completed: November  9, 2005, 19:18:31
Job time : 1772 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 9, 2005, 18:06:40 ; Search time 94 Seconds
(without alignments)
382.958 Million cell updates/sec

Title: US-09-937-057-9
Perfect score: 22
Sequence: 1 tgactgtgaacgttatagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1330268

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20.4	92.7	22	3	US-09-092-314-2	Sequence 2, Appli
2	20.4	92.7	22	4	US-09-791-500-5	Sequence 5, Appli
3	20.4	92.7	22	4	US-09-791-500-6	Sequence 6, Appli
4	18.8	85.5	22	3	US-09-092-314-1	Sequence 1, Appli
5	18.8	85.5	22	3	US-09-092-314-3	Sequence 3, Appli
6	18.8	85.5	22	3	US-09-092-314-10	Sequence 10, Appl
7	18.8	85.5	22	4	US-09-235-742-19	Sequence 19, Appl
8	18.8	85.5	22	4	US-09-347-343-32	Sequence 32, Appl
9	18.8	85.5	22	4	US-09-347-343-33	Sequence 33, Appl
10	18.8	85.5	22	4	US-09-820-484-1	Sequence 1, Appli
11	18.8	85.5	22	4	US-09-820-484-3	Sequence 3, Appli
12	18.8	85.5	22	4	US-09-820-484-7	Sequence 7, Appli
13	18.8	85.5	22	4	US-09-774-403A-1	Sequence 1, Appli
14	18.8	85.5	22	4	US-09-774-403A-3	Sequence 3, Appli
15	18.8	85.5	22	4	US-09-296-477-2	Sequence 2, Appli
16	18.8	85.5	22	4	US-09-296-477-3	Sequence 3, Appli
17	18.8	85.5	22	4	US-09-296-477-6	Sequence 6, Appli
18	18.8	85.5	22	4	US-09-296-477-8	Sequence 8, Appli
19	18.8	85.5	22	4	US-09-308-036A-1	Sequence 1, Appli
20	18.8	85.5	22	4	US-09-791-500-1	Sequence 1, Appli
21	18.8	85.5	22	4	US-09-791-500-3	Sequence 3, Appli
22	18.8	85.5	22	4	US-09-791-500-8	Sequence 8, Appli
23	18.8	85.5	22	4	US-09-565-906-2	Sequence 2, Appli
24	18.4	83.6	22	4	US-09-296-477-16	Sequence 16, Appl
25	17.8	80.9	22	4	US-09-296-477-12	Sequence 12, Appl
26	17.8	80.9	22	4	US-09-296-477-15	Sequence 15, Appl
27	17.2	78.2	22	3	US-09-092-314-4	Sequence 4, Appli
28	17.2	78.2	22	4	US-09-235-742-20	Sequence 20, Appl
29	17.2	78.2	22	4	US-09-820-484-2	Sequence 2, Appli
30	17.2	78.2	22	4	US-09-820-484-6	Sequence 6, Appli
31	17.2	78.2	22	4	US-09-774-403A-2	Sequence 2, Appli
32	17.2	78.2	22	4	US-09-296-477-1	Sequence 1, Appli
c 33	17.2	78.2	22	4	US-09-296-477-5	Sequence 5, Appli
34	17.2	78.2	22	4	US-09-296-477-9	Sequence 9, Appli
35	17.2	78.2	22	4	US-09-296-477-13	Sequence 13, Appl
36	17.2	78.2	22	4	US-09-308-036A-2	Sequence 2, Appli
37	17.2	78.2	22	4	US-09-791-500-4	Sequence 4, Appli
38	17.2	78.2	22	4	US-09-791-500-9	Sequence 9, Appli
39	15.6	70.9	22	3	US-09-092-314-5	Sequence 5, Appli
40	15.6	70.9	22	3	US-09-092-314-7	Sequence 7, Appli
41	15.6	70.9	22	3	US-09-092-314-8	Sequence 8, Appli
42	15.6	70.9	22	4	US-09-791-500-2	Sequence 2, Appli
43	15.4	70.0	21	4	US-09-296-477-10	Sequence 10, Appl
44	15.4	70.0	23	4	US-09-296-477-11	Sequence 11, Appl
c 45	14.8	67.3	25	4	US-09-396-196G-55466	Sequence 55466, A

ALIGNMENTS

RESULT 1
US-09-092-314-2
; Sequence 2, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Roman, Mark
; TITLE OF INVENTION: Inhibitors of DNA Immunostimulatory
; TITLE OF INVENTION: Sequence Activity
; Patent No. 6225292
; FILE REFERENCE: 6510-173US1
; CURRENT APPLICATION NUMBER: US/09/092,314
; CURRENT FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/048,794
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-092-314-2

Query Match 92.7%; Score 20.4; DB 3; Length 22;
Best Local Similarity 95.5%; Pred. No. 1;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22
```

RESULT 2
US-09-791-500-5
; Sequence 5, Application US/09791500
; Patent No. 6613751
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202US1
; CURRENT APPLICATION NUMBER: US/09/791,500
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-5

  Query Match             92.7%;  Score 20.4;  DB 4;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 1;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 3
US-09-791-500-6
; Sequence 6, Application US/09791500
; Patent No. 6613751
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Rachmilewitz, Daniel
;  TITLE OF INVENTION: Method for Treating Inflammatory Bowel
;  TITLE OF INVENTION:  Disease and Other Forms of Gastrointestinal Inflammation.
;  FILE REFERENCE: 6510-202US1
;  CURRENT APPLICATION NUMBER: US/09/791,500
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-6

  Query Match             92.7%;  Score 20.4;  DB 4;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 1;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 4
US-09-092-314-1
; Sequence 1, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
;  APPLICANT:  Raz, Eyal
;  APPLICANT:  Roman, Mark
;  TITLE OF INVENTION:  Inhibitors of DNA Immunostimulatory
;  TITLE OF INVENTION:  Sequence Activity
; Patent No. 6225292
;  FILE REFERENCE:  6510-173US1
;  CURRENT APPLICATION NUMBER: US/09/092,314
;  CURRENT FILING DATE:  1998-06-05
;  PRIOR APPLICATION NUMBER:  60/048,794
;  PRIOR FILING DATE:  1997-06-06
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-092-314-1

  Query Match             85.5%;  Score 18.8;  DB 3;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.3;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||| |||| ||||||
Db          1 TGACTGTGAAGGTTAGAGATGA 22


RESULT 5
US-09-092-314-3
; Sequence 3, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
;  APPLICANT:  Raz, Eyal
;  APPLICANT:  Roman, Mark
;  TITLE OF INVENTION:  Inhibitors of DNA Immunostimulatory
;  TITLE OF INVENTION:  Sequence Activity
; Patent No. 6225292
;  FILE REFERENCE:  6510-173US1
;  CURRENT APPLICATION NUMBER: US/09/092,314
;  CURRENT FILING DATE:  1998-06-05
;  PRIOR APPLICATION NUMBER:  60/048,794
;  PRIOR FILING DATE:  1997-06-06
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-092-314-3

  Query Match             85.5%;  Score 18.8;  DB 3;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.3;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||| ||| ||||||
Db          1 TGACTGTGAACCTTAGAGATGA 22


RESULT 6
US-09-092-314-10
; Sequence 10, Application US/09092314
; Patent No. 6225292
; GENERAL INFORMATION:
;  APPLICANT:  Raz, Eyal
;  APPLICANT:  Roman, Mark
;  TITLE OF INVENTION:  Inhibitors of DNA Immunostimulatory
;  TITLE OF INVENTION:  Sequence Activity
; Patent No. 6225292
;  FILE REFERENCE:  6510-173US1
;  CURRENT APPLICATION NUMBER: US/09/092,314
;  CURRENT FILING DATE:  1998-06-05
;  PRIOR APPLICATION NUMBER:  60/048,794
;  PRIOR FILING DATE:  1997-06-06
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide
US-09-092-314-10

  Query Match             85.5%;  Score 18.8;  DB 3;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.3;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||| |||| ||||||
Db          1 TGACTGTGAATGTTAGAGATGA 22
```

```
RESULT 7
US-09-235-742-19
; Sequence 19, Application US/09235742
; Patent No. 6498148
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  TITLE OF INVENTION: Immunization-Free Methods for Treating
;  TITLE OF INVENTION: Antigen-Stimulated Inflammation in a Mammalian Host and
;  TITLE OF INVENTION: Shifting the Host's Antigen Immune Responsiveness to a TH1
;  TITLE OF INVENTION: Phenotype
;  FILE REFERENCE: 6510-170CON4
;  CURRENT APPLICATION NUMBER: US/09/235,742
;  CURRENT FILING DATE: 1999-01-21
;  EARLIER APPLICATION NUMBER: 08/927,120
;  EARLIER FILING DATE: 1997-09-05
;  EARLIER APPLICATION NUMBER: 08/593,554
;  EARLIER FILING DATE: 1996-01-30
;  EARLIER APPLICATION NUMBER: 08/725,968
;  EARLIER FILING DATE: 1996-10-04
;  EARLIER APPLICATION NUMBER: 60/028,118
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Recombinant or Synthetic Sequence
US-09-235-742-19

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.3;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||  ||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 8
US-09-347-343-32
; Sequence 32, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
;  APPLICANT: RAZ, Eyal R.
;  APPLICANT: KOBAYASHI, Hiroko
;  TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
;  FILE REFERENCE: 30448.64US01
;  CURRENT APPLICATION NUMBER: US/09/347,343A
;  CURRENT FILING DATE: 1999-07-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: synthetic oligonucleotide
US-09-347-343-32

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.3;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||  ||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 9
US-09-347-343-33
; Sequence 33, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
;  APPLICANT: RAZ, Eyal R.
;  APPLICANT: KOBAYASHI, Hiroko
;  TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
;  FILE REFERENCE: 30448.64US01
;  CURRENT APPLICATION NUMBER: US/09/347,343A
;  CURRENT FILING DATE: 1999-07-02
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: synthetic oligonucleotide
US-09-347-343-33

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.3;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||| ||| ||||||
Db          1 TGACTGTGAACCTTAGAGATGA 22


RESULT 10
US-09-820-484-1
; Sequence 1, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203;567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
;   NAME/KEY: modified_base
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: disulfide thymine
US-09-820-484-1

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.3;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||  ||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 11
US-09-820-484-3
; Sequence 3, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
```

```
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: phosphorothioate ISS-ODN
US-09-820-484-3

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.3;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||  ||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 12
US-09-820-484-7
; Sequence 7, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
;  APPLICANT: Raz, Eyal
;  APPLICANT:  Cho, Hearn Jay
;  APPLICANT:  Richman, Douglas
;  APPLICANT:  Horner, Anthony A.
;  TITLE OF INVENTION: Method for Increasing a Cytotoxic T
;  TITLE OF INVENTION:  Lymphocyte Response in vivo.
;  FILE REFERENCE: 06510-188US1
;  CURRENT APPLICATION NUMBER: US/09/820,484
;  CURRENT FILING DATE:  2001-03-28
;  PRIOR APPLICATION NUMBER: US 60/192,537
;  PRIOR FILING DATE: 2000-03-28
;  PRIOR APPLICATION NUMBER: US 60/203,567
;  PRIOR FILING DATE: 2000-05-11
;  PRIOR APPLICATION NUMBER: US 60/215,895
;  PRIOR FILING DATE: 2000-07-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mODN
US-09-820-484-7

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.3;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||| ||| ||||||
Db          1 TGACTGTGAACCTTAGAGATGA 22


RESULT 13
US-09-774-403A-1
; Sequence 1, Application US/09774403A
; Patent No. 6552006
; GENERAL INFORMATION:
;  APPLICANT: Eyal Raz
;  APPLICANT:  Richard Kornbluth
;  APPLICANT:  Antonio Catanzaro
;  APPLICANT:  Tomoko Hayashi
;  APPLICANT:  Dennis Carson
;  TITLE OF INVENTION: Immunomodulatory Polynucleotides in
;  TITLE OF INVENTION:  Treatment of Infection by an Intracellular Pathogen
;  FILE REFERENCE: UCAL166
;  CURRENT APPLICATION NUMBER: US/09/774,403A
;  CURRENT FILING DATE:  2002-04-15
;  PRIOR APPLICATION NUMBER: 60/179,353
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Immunomodulatory sequence
US-09-774-403A-1

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.3;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||  ||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 14
US-09-774-403A-3
; Sequence 3, Application US/09774403A
; Patent No. 6552006
; GENERAL INFORMATION:
;  APPLICANT: Eyal Raz
;  APPLICANT:  Richard Kornbluth
;  APPLICANT:  Antonio Catanzaro
;  APPLICANT:  Tomoko Hayashi
;  APPLICANT:  Dennis Carson
;  TITLE OF INVENTION: Immunomodulatory Polynucleotides in
;  TITLE OF INVENTION:  Treatment of Infection by an Intracellular Pathogen
;  FILE REFERENCE: UCAL166
;  CURRENT APPLICATION NUMBER: US/09/774,403A
;  CURRENT FILING DATE:  2002-04-15
;  PRIOR APPLICATION NUMBER: 60/179,353
;  PRIOR FILING DATE: 2000-01-31
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Control sequence
US-09-774-403A-3

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.3;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||| |||| ||||||
Db          1 TGACTGTGAAGGTTAGAGATGA 22


RESULT 15
US-09-296-477-2
```

```
; Sequence 2, Application US/09296477A
; Patent No. 6589940
; GENERAL INFORMATION:
;  APPLICANT: RAZ, E.
;  APPLICANT: SCHWARTZ, D.
;  APPLICANT: ROMAN, M.
;  APPLICANT: DINA, D.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES,
;  TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF USE
;  TITLE OF INVENTION: THEREOF
;  FILE REFERENCE: 377882000420
;  CURRENT APPLICATION NUMBER: US/09/296,477A
;  CURRENT FILING DATE: 1999-04-22
;  EARLIER APPLICATION NUMBER: 09/092,329
;  EARLIER FILING DATE: 1998-06-05
;  EARLIER APPLICATION NUMBER: 60/048,793
;  EARLIER FILING DATE: 1997-06-06
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic construct
US-09-296-477-2

  Query Match             85.5%;  Score 18.8;  DB 4;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.3;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||  ||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


Search completed: November  9, 2005, 19:20:07
Job time : 96 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 9, 2005, 17:34:52 ; Search time 1718 Seconds
(without alignments)
620.498 Million cell updates/sec

Title: US-09-937-057-9
Perfect score: 22
Sequence: 1 tgactgtgaacgttatagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 2238514

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	22	6	BD272064	BD272064 Use of st
2	22	100.0	22	6	AX036952	AX036952 Sequence
3	20.4	92.7	22	6	AR148608	AR148608 Sequence
4	20.4	92.7	22	6	BD136175	BD136175 Inhibitor
5	20.4	92.7	22	6	AR392166	AR392166 Sequence
6	20.4	92.7	22	6	AR392167	AR392167 Sequence
7	18.8	85.5	22	6	AR148607	AR148607 Sequence
8	18.8	85.5	22	6	AR148609	AR148609 Sequence
9	18.8	85.5	22	6	AR148616	AR148616 Sequence
10	18.8	85.5	22	6	BD136174	BD136174 Inhibitor
11	18.8	85.5	22	6	BD136176	BD136176 Inhibitor
12	18.8	85.5	22	6	BD136183	BD136183 Inhibitor
13	18.8	85.5	22	6	BD182369	BD182369 Anti-tumo
14	18.8	85.5	22	6	BD185615	BD185615 Anti-tumo
15	18.8	85.5	22	6	BD190435	BD190435 Microemul
16	18.8	85.5	22	6	BD190436	BD190436 Microemul
17	18.8	85.5	22	6	BD228690	BD228690 Methods a
18	18.8	85.5	22	6	BD228691	BD228691 Methods a
19	18.8	85.5	22	6	BD233617	BD233617 Immunosti
20	18.8	85.5	22	6	BD233618	BD233618 Immunosti
21	18.8	85.5	22	6	BD233621	BD233621 Immunosti
22	18.8	85.5	22	6	BD233623	BD233623 Immunosti
23	18.8	85.5	22	6	BD251283	BD251283 Enhanceme
24	18.8	85.5	22	6	BD251284	BD251284 Enhanceme
25	18.8	85.5	22	6	BD272056	BD272056 Use of st
26	18.8	85.5	22	6	BD272057	BD272057 Use of st
27	18.8	85.5	22	6	BD272058	BD272058 Use of st
28	18.8	85.5	22	6	AR268334	AR268334 Sequence
29	18.8	85.5	22	6	AR287741	AR287741 Sequence
30	18.8	85.5	22	6	AR287743	AR287743 Sequence
31	18.8	85.5	22	6	AR287745	AR287745 Sequence
32	18.8	85.5	22	6	AR308057	AR308057 Sequence
33	18.8	85.5	22	6	AR308059	AR308059 Sequence
34	18.8	85.5	22	6	AR352573	AR352573 Sequence
35	18.8	85.5	22	6	AR352574	AR352574 Sequence
36	18.8	85.5	22	6	AR352577	AR352577 Sequence
37	18.8	85.5	22	6	AR352579	AR352579 Sequence
38	18.8	85.5	22	6	AR383158	AR383158 Sequence
39	18.8	85.5	22	6	AR392162	AR392162 Sequence
40	18.8	85.5	22	6	AR392164	AR392164 Sequence
41	18.8	85.5	22	6	AR392169	AR392169 Sequence
42	18.8	85.5	22	6	AR535277	AR535277 Sequence
43	18.8	85.5	22	6	AX036944	AX036944 Sequence
44	18.8	85.5	22	6	AX036945	AX036945 Sequence
45	18.8	85.5	22	6	AX036946	AX036946 Sequence

ALIGNMENTS

RESULT 1
BD272064
LOCUS BD272064 22 bp DNA linear PAT 17-JUL-2003
DEFINITION Use of stabilized oligonucleotide for producing agents having antitumor activity.
ACCESSION BD272064
VERSION BD272064.1 GI:33081832
KEYWORDS JP 2002539265-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Carpentier,A.
TITLE Use of stabilized oligonucleotide for producing agents having antitumor activity
JOURNAL Patent: JP 2002539265-A 9 19-NOV-2002;
ASSISTANCE PUBLIQUE HOPITAUX DE PARIS, INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE (INSERM)
COMMENT OS Artificial Sequence
PN JP 2002539265-A/9
PD 19-NOV-2002
PF 17-MAR-2000 JP 2000606246
PR 19-MAR-1999 FR 99/03433
PI ANTOINE CARPENTIER
PC A61K47/48,A61K31/711,A61P35/00
CC Description of the Artificial Sequence: oligodeoxynucleotide
FH Key Location/Qualifiers
FT source 1. .22
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||||||||||||

```
Db          1 TGACTGTGAACGTTATAGATGA 22


RESULT 2
AX036952
LOCUS       AX036952                  22 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 9 from Patent FR2790955.
ACCESSION   AX036952
VERSION     AX036952.1  GI:11226380
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Carpentier,A.
  JOURNAL   Patent: FR 2790955-A 9 22-SEP-2000;
            ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligodesoxynucleotide"
ORIGIN

  Query Match           100.0%;  Score 22;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1.1;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTATAGATGA 22


RESULT 3
AR148608
LOCUS       AR148608                  22 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6225292.
ACCESSION   AR148608
VERSION     AR148608.1  GI:15112698
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E. and Roman,M.
  TITLE     Inhibitors of DNA immunostimulatory sequence activity
  JOURNAL   Patent: US 6225292-A 2 01-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           92.7%;  Score 20.4;  DB 6;  Length 22;
  Best Local Similarity  95.5%;  Pred. No. 7.7;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 4
BD136175
LOCUS       BD136175                  22 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Inhibitors of DNA immunostimulatory sequence activity.
ACCESSION   BD136175
VERSION     BD136175.1  GI:23231120
KEYWORDS    JP 2002505580-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E. and Roman,M.
  TITLE     Inhibitors of DNA immunostimulatory sequence activity
  JOURNAL   Patent: JP 2002505580-A 2 19-FEB-2002;
            DYNAVAX TECHNOLOGIES CORP, THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA
COMMENT     OS   Artificial Sequence
            PN   JP 2002505580-A/2
            PD   19-FEB-2002
            PF   05-JUN-1998 JP 1999502803
            PR   06-JUN-1997 US    60/048793
            PI   EYAL RAZ,MARK ROMAN
            PC   C12N15/00,C12N15/63,C12N15/79,C12N15/09,A61K48/00 CC
            Oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           92.7%;  Score 20.4;  DB 6;  Length 22;
  Best Local Similarity  95.5%;  Pred. No. 7.7;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 5
AR392166
LOCUS       AR392166                  22 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 5 from patent US 6613751.
ACCESSION   AR392166
VERSION     AR392166.1  GI:40116143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E. and Rachmilewitz,D.
  TITLE     Method for treating inflammatory bowel disease and other forms of
            gastrointestinal inflammation
  JOURNAL   Patent: US 6613751-A 5 02-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           92.7%;  Score 20.4;  DB 6;  Length 22;
  Best Local Similarity  95.5%;  Pred. No. 7.7;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 6
AR392167
LOCUS       AR392167                  22 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6613751.
ACCESSION   AR392167
VERSION     AR392167.1  GI:40116144
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

```
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E. and Rachmilewitz,D.
  TITLE     Method for treating inflammatory bowel disease and other forms of
            gastrointestinal inflammation
  JOURNAL   Patent: US 6613751-A 6 02-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             92.7%;  Score 20.4;  DB 6;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 7.7;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 7
AR148607
LOCUS       AR148607                  22 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6225292.
ACCESSION   AR148607
VERSION     AR148607.1  GI:15112697
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E. and Roman,M.
  TITLE     Inhibitors of DNA immunostimulatory sequence activity
  JOURNAL   Patent: US 6225292-A 1 01-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 55;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||| |||| ||||||
Db          1 TGACTGTGAAGGTTAGAGATGA 22


RESULT 8
AR148609
LOCUS       AR148609                  22 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 3 from patent US 6225292.
ACCESSION   AR148609
VERSION     AR148609.1  GI:15112699
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E. and Roman,M.
  TITLE     Inhibitors of DNA immunostimulatory sequence activity
  JOURNAL   Patent: US 6225292-A 3 01-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 55;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||| ||| ||||||
Db          1 TGACTGTGAACCTTAGAGATGA 22


RESULT 9
AR148616
LOCUS       AR148616                  22 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 10 from patent US 6225292.
ACCESSION   AR148616
VERSION     AR148616.1  GI:15112706
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E. and Roman,M.
  TITLE     Inhibitors of DNA immunostimulatory sequence activity
  JOURNAL   Patent: US 6225292-A 10 01-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 55;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||| |||| ||||||
Db          1 TGACTGTGAATGTTAGAGATGA 22


RESULT 10
BD136174
LOCUS       BD136174                  22 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Inhibitors of DNA immunostimulatory sequence activity.
ACCESSION   BD136174
VERSION     BD136174.1  GI:23231119
KEYWORDS    JP 2002505580-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E. and Roman,M.
  TITLE     Inhibitors of DNA immunostimulatory sequence activity
  JOURNAL   Patent: JP 2002505580-A 1 19-FEB-2002;
            DYNAVAX TECHNOLOGIES CORP, THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA
COMMENT     OS   Artificial Sequence
            PN   JP 2002505580-A/1
            PD   19-FEB-2002
            PF   05-JUN-1998 JP 1999502803
            PR   06-JUN-1997 US    60/048793
            PI   EYAL RAZ,MARK ROMAN
            PC   C12N15/00,C12N15/63,C12N15/79,C12N15/09,A61K48/00 CC
            Oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 55;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
```

```
              ||||||||||| |||| ||||||
Db          1 TGACTGTGAAGGTTAGAGATGA 22


RESULT 11
BD136176
LOCUS       BD136176                 22 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Inhibitors of DNA immunostimulatory sequence activity.
ACCESSION   BD136176
VERSION     BD136176.1  GI:23231121
KEYWORDS    JP 2002505580-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E. and Roman,M.
  TITLE     Inhibitors of DNA immunostimulatory sequence activity
  JOURNAL   Patent: JP 2002505580-A 3 19-FEB-2002;
            DYNAVAX TECHNOLOGIES CORP, THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA
COMMENT     OS   Artificial Sequence
            PN   JP 2002505580-A/3
            PD   19-FEB-2002
            PF   05-JUN-1998 JP 1999502803
            PR   06-JUN-1997 US    60/048793
            PI   EYAL RAZ,MARK ROMAN
            PC   C12N15/00,C12N15/63,C12N15/79,C12N15/09,A61K48/00 CC
            Oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 55;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||  ||| ||||||
Db          1 TGACTGTGAACCTTAGAGATGA 22


RESULT 12
BD136183
LOCUS       BD136183                 22 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Inhibitors of DNA immunostimulatory sequence activity.
ACCESSION   BD136183
VERSION     BD136183.1  GI:23231128
KEYWORDS    JP 2002505580-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Raz,E. and Roman,M.
  TITLE     Inhibitors of DNA immunostimulatory sequence activity
  JOURNAL   Patent: JP 2002505580-A 10 19-FEB-2002;
            DYNAVAX TECHNOLOGIES CORP, THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA
COMMENT     OS   Artificial Sequence
            PN   JP 2002505580-A/10
            PD   19-FEB-2002
            PF   05-JUN-1998 JP 1999502803
            PR   06-JUN-1997 US    60/048793
            PI   EYAL RAZ,MARK ROMAN
            PC   C12N15/00,C12N15/63,C12N15/79,C12N15/09,A61K48/00 CC
            Oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 55;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||| ||||| ||||||
Db          1 TGACTGTGAATGTTAGAGATGA 22


RESULT 13
BD182369
LOCUS       BD182369                 22 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Anti-tumor antigens or their epitopes against HTLV-1 tumor.
ACCESSION   BD182369
VERSION     BD182369.1  GI:30793287
KEYWORDS    WO 02090981-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hanabuchi,S., Ohashi,T. and Kannagi,M.
  TITLE     Anti-tumor antigens or their epitopes against HTLV-1 tumor
  JOURNAL   Patent: WO 02090981-A 1 14-NOV-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP,SHINO HANABUCHI,TAKASHI OHASHI,
            MARI KANNAGI
COMMENT     OS   Artificial Sequence
            PN   WO 02090981-A/1
            PD   14-NOV-2002
            PF   02-MAY-2002 WO 2002JP004406
            PR   08-MAY-2001 JP 01P   137526
            PI   SHINO HANABUCHI,TAKASHI OHASHI,MARI KANNAGI
            PC   G01N33/50,G01N33/15,A61K39/00
            CC   Description of Artificial Sequence:ISS-ODN
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             85.5%;  Score 18.8;  DB 6;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 55;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||  ||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 14
BD185615
LOCUS       BD185615                 22 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Anti-tumor antigens or their epitopes against HTLV-I tumor.
ACCESSION   BD185615
VERSION     BD185615.1  GI:31877815
KEYWORDS    JP 2002372532-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hanabuchi,S., Ohashi,T. and Kannagi,M.
  TITLE     Anti-tumor antigens or their epitopes against HTLV-I tumor
```

```
  JOURNAL   Patent: JP 2002372532-A 1 26-DEC-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002372532-A/1
            PD   26-DEC-2002
            PF   08-MAY-2001 JP 2001137526
            PI   SHINO HANABUCHI,TAKASHI OHASHI,MARI KANNAGI
            PC   G01N33/50,A61K39/00,A61K39/21,A61P35/00,A61P35/02,A61P37/04,
            PC   C07K7/06,
            PC   C12N5/06,C12Q1/02,G01N33/00,G01N33/15,G01N33/53,G01N33/53, PC
             G01N33/566,
            PC   G01N33/574
            CC   Description of Artificial Sequence:ISS-ODN
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .22
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
ORIGIN

  Query Match            85.5%;  Score 18.8;  DB 6;  Length 22;
  Best Local Similarity  90.9%;  Pred. No. 55;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||  ||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


RESULT 15
BD190435
LOCUS       BD190435                 22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Microemulsions with Adsorbed Macromoelecules and Microparticles.
ACCESSION   BD190435
VERSION     BD190435.1  GI:33000174
KEYWORDS    JP 2002537102-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Barackman,J., Simph,M., Ugozoli,M., Kazazu,J., Donnelly,J.,
            Ott,G.S. and Ohagan,D.
  TITLE     Microemulsions with Adsorbed Macromoelecules and Microparticles
  JOURNAL   Patent: JP 2002537102-A 19 05-NOV-2002;
            Chiron Corporation
COMMENT     OS   Artificial Sequence
            PN   JP 2002537102-A/19
            PD   05-NOV-2002
            PF   09-FEB-2000 JP 2000600618
            PR   29-JUL-1999 US    60/146391,28-OCT-1999 US    60/161997, PR
            26-FEB-1999 US    60/121858
            PI   john barackman,manmohan simph,mildred ugozoli,jina kazazu,john

            PI   donnelly,
            PI   gary s ott,derek ohagan
            CC   Oligonucleotide
            FH   Key             Location/Qualifiers.
FEATURES            Location/Qualifiers
     source         1. .22
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"
ORIGIN

  Query Match            85.5%;  Score 18.8;  DB 6;  Length 22;
  Best Local Similarity  90.9%;  Pred. No. 55;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||  ||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


Search completed: November  9, 2005, 18:48:51
Job time : 1724 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 9, 2005, 17:05:55 ; Search time 269 Seconds
(without alignments)
484.142 Million cell updates/sec

Title: US-09-937-057-9
Perfect score: 22
Sequence: 1 tgactgtgaacgttatagatga 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4530610

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	100.0	22	3	AAA96260	Aaa96260 Sequence
2	20.4	92.7	22	4	AAH43343	Aah43343 Immunomod
3	20.4	92.7	22	4	AAH43342	Aah43342 Immunomod
4	20.4	92.7	22	6	AAD24895	Aad24895 Methylate
5	20.4	92.7	22	6	AAD24894	Aad24894 Immunosti
6	20.4	92.7	22	12	ADO55351	Ado55351 Immune mo
7	19.4	88.2	22	12	ADO55287	Ado55287 Immune mo
8	18.8	85.5	22	2	AAV32079	Aav32079 Nucleotid
9	18.8	85.5	22	2	AAV80099	Aav80099 Immunomod
10	18.8	85.5	22	2	AAV80097	Aav80097 Immunomod
11	18.8	85.5	22	2	AAV80103	Aav80103 Immunomod
12	18.8	85.5	22	2	AAV80106	Aav80106 Oligo use
13	18.8	85.5	22	2	AAV80101	Aav80101 Immunomod
14	18.8	85.5	22	2	AAV80104	Aav80104 Oligo use
15	18.8	85.5	22	2	AAV80102	Aav80102 Immunomod
16	18.8	85.5	22	2	AAV55797	Aav55797 Immunosti
17	18.8	85.5	22	2	AAV55788	Aav55788 Immunosti
18	18.8	85.5	22	2	AAV55790	Aav55790 Immunosti
19	18.8	85.5	22	2	AAX36624	Aax36624 ISS-ODN D
20	18.8	85.5	22	3	AAA14469	Aaa14469 Mutant im
21	18.8	85.5	22	3	AAA14467	Aaa14467 Immunosti
22	18.8	85.5	22	3	AAA38072	Aaa38072 Immunosti
23	18.8	85.5	22	3	AAA38070	Aaa38070 Immunosti
24	18.8	85.5	22	3	AAA38068	Aaa38068 Immunosti
25	18.8	85.5	22	3	AAA38071	Aaa38071 Immunosti
26	18.8	85.5	22	3	AAA38065	Aaa38065 Immunosti
27	18.8	85.5	22	3	AAA90459	Aaa90459 CpG adjuv
28	18.8	85.5	22	3	AAA90458	Aaa90458 CpG adjuv
29	18.8	85.5	22	3	AAA96254	Aaa96254 Sequence
30	18.8	85.5	22	3	AAA96253	Aaa96253 Sequence
31	18.8	85.5	22	3	AAA96252	Aaa96252 Sequence
32	18.8	85.5	22	3	AAZ55876	Aaz55876 Immunomod
33	18.8	85.5	22	3	AAC64052	Aac64052 Non-CpG c
34	18.8	85.5	22	3	AAC64051	Aac64051 Immunosti
35	18.8	85.5	22	4	AAH20404	Aah20404 CpG motif
36	18.8	85.5	22	4	AAH20403	Aah20403 CpG motif
37	18.8	85.5	22	4	AAH43345	Aah43345 Immunomod
38	18.8	85.5	22	4	AAH43340	Aah43340 Immunomod
39	18.8	85.5	22	4	AAH43338	Aah43338 Immunomod
40	18.8	85.5	22	4	AAH73439	Aah73439 Immunomod
41	18.8	85.5	22	4	AAH73441	Aah73441 Immunomod
42	18.8	85.5	22	4	AAH75992	Aah75992 Immunomod
43	18.8	85.5	22	4	AAI64301	Aai64301 Control o
44	18.8	85.5	22	4	AAH75995	Aah75995 Immunomod
45	18.8	85.5	22	4	AAH76000	Aah76000 Control o

ALIGNMENTS

RESULT 1
AAA96260
ID AAA96260 standard; DNA; 22 BP.
XX
AC AAA96260;
XX
DT 08-FEB-2001 (first entry)
XX
DE Sequence of a stabilised oligonucleotide with antitumour activity.
XX
KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
KW glioblastoma; medullablastoma; neuroblastoma; melanoma; carcinoma; ss.
XX
OS Synthetic.
XX
PN WO200056342-A2.
XX
PD 28-SEP-2000.
XX
PF 17-MAR-2000; 2000WO-FR000676.
XX
PR 19-MAR-1999; 99FR-00003433.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
XX
PI Carpentier A;
XX
DR WPI; 2000-602192/57.
XX
PT Use of stabilized oligonucleotides as antitumor agents, particularly
PT against nervous system tumors, have optimal activity and are not toxic.
XX
PS Claim 3; Page 48; 57pp; French.
XX
CC The present sequence represents a stabilised oligonucleotide which has
CC antitumour activity. The oligonucleotide comprises an octomer motif of
CC the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where the pair
CC X-X is AT, AA, CT or TT. The oligonucleotides are immunostimulatory, and
CC are not toxic. They may be adapted for use in animals or humans. The
CC stabilised oligonucleotides are used for treating tumours, of any type
CC and any degree of anaplasia, particularly human tumours in the peripheral
CC or central nervous systems, specifically glioblastomas, medullablastomas,

```
CC   neuroblastomas, melanomas or carcinomas
XX
SQ   Sequence 22 BP; 7 A; 2 C; 6 G; 7 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 22;  DB 3;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 0.65;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||||||||||
Db          1 TGACTGTGAACGTTATAGATGA 22


RESULT 2
AAH43343
ID   AAH43343 standard; DNA; 22 BP.
XX
AC   AAH43343;
XX
DT   13-DEC-2001  (first entry)
XX
DE   Immunomodulatory polynucleotide 1039.
XX
KW   Immunomodulation; inflammation; gastrointestinal tract;
KW   ulcerative colitis; Crohn's disease; inflammatory bowel disease;
KW   diarrhoea; rectal bleeding; weight loss; colon; weight; lesion; ss.
XX
OS   Synthetic.
XX
PN   WO200162207-A2.
XX
PD   30-AUG-2001.
XX
PF   22-FEB-2001; 2001WO-US006034.
XX
PR   23-FEB-2000; 2000US-0184256P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Raz E,  Rachmilewitz D;
XX
DR   WPI; 2001-565393/63.
XX
PT   Ameliorating gastrointestinal inflammation e.g. inflammatory bowel
PT   disease involves administering an immunomodulatory nucleic acid.
XX
PS   Example 2; Page 28; 58pp; English.
XX
CC   The sequences given in AAH43338-48 represent immunomodulatory
CC   polynucleotides which may be used to ameliorate inflammation of the
CC   gastrointestinal tract by administering a nucleic acid comprising one of
CC   these sequences. These polynucleotides all comprise an immunomodulatory
CC   nucleotide sequence of 5'-CpG-3' (I). The nucleotides may be used for
CC   ameliorating or reducing gastrointestinal inflammation e.g. chronic or
CC   acute gastrointestinal inflammation, ulcerative colitis, Crohn's disease
CC   caused by inflammatory bowel disease; diarrhoea, rectal bleeding, weight
CC   loss; to reduce colon weight and colon lesions; to reduce a colonic
CC   inflammation. The immunomodulatory polynucleotides treat inflammatory
CC   bowel disease satisfactorily and effectively and have little or no
CC   toxicity even at a high dosage of 50000 micro-g. They also reduce the
CC   risk of colonic cancer by treating ulcerative colitis
XX
SQ   Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match            92.7%;  Score 20.4;  DB 4;  Length 22;
  Best Local Similarity  95.5%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 3
AAH43342
ID   AAH43342 standard; DNA; 22 BP.
XX
AC   AAH43342;
XX
DT   13-DEC-2001  (first entry)
XX
DE   Immunomodulatory polynucleotide 1038.
XX
KW   Immunomodulation; inflammation; gastrointestinal tract;
KW   ulcerative colitis; Crohn's disease; inflammatory bowel disease;
KW   diarrhoea; rectal bleeding; weight loss; colon; weight; lesion; ss.
XX
OS   Synthetic.
XX
PN   WO200162207-A2.
XX
PD   30-AUG-2001.
XX
PF   22-FEB-2001; 2001WO-US006034.
XX
PR   23-FEB-2000; 2000US-0184256P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Raz E,  Rachmilewitz D;
XX
DR   WPI; 2001-565393/63.
XX
PT   Ameliorating gastrointestinal inflammation e.g. inflammatory bowel
PT   disease involves administering an immunomodulatory nucleic acid.
XX
PS   Claim 7; Page 28; 58pp; English.
XX
CC   The sequences given in AAH43338-48 represent immunomodulatory
CC   polynucleotides which may be used to ameliorate inflammation of the
CC   gastrointestinal tract by administering a nucleic acid comprising one of
CC   these sequences. These polynucleotides all comprise an immunomodulatory
CC   nucleotide sequence of 5'-CpG-3' (I). The nucleotides may be used for
CC   ameliorating or reducing gastrointestinal inflammation e.g. chronic or
CC   acute gastrointestinal inflammation, ulcerative colitis, Crohn's disease
CC   caused by inflammatory bowel disease; diarrhoea, rectal bleeding, weight
CC   loss; to reduce colon weight and colon lesions; to reduce a colonic
CC   inflammation. The immunomodulatory polynucleotides treat inflammatory
CC   bowel disease satisfactorily and effectively and have little or no
CC   toxicity even at a high dosage of 50000 micro-g. They also reduce the
CC   risk of colonic cancer by treating ulcerative colitis
XX
SQ   Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match            92.7%;  Score 20.4;  DB 4;  Length 22;
  Best Local Similarity  95.5%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 4
AAD24895
ID   AAD24895 standard; DNA; 22 BP.
XX
AC   AAD24895;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Methylated (5-methyl C) immunostimulatory oligodeoxynucleotide (ISS-ODN).
XX
KW   Cell death; DNA damage; DNA-dependent protein kinase; DNA-PK; necrosis;
KW   immune response; apoptosis; Alzheimer's disease; Parkinson's disease;
KW   rheumatoid arthritis; inflammation; osteoporosis; myocardial infarction;
```

```
KW   liver disease; reperfusion injury; carcinoma; multiple sclerosis; stroke;
KW   amyotrophic lateral sclerosis; Acquired Immune Deficiency Syndrome; AIDS;
KW   head injury damage; aplastic anaemia; tumour; organ transplantation;
KW   cerebral infarction; follicular lymphomas; systemic lupus erythematosus;
KW   viral infection; glomerulonephritis; apoptosis; autoimmune disorder;
KW   sepsis; immunostimulatory oligodeoxynucleotide; ISS-ODN; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   modified_base    11
FT                    /*tag=  a
FT                    /mod_base= m5c
XX
PN   WO200185910-A2.
XX
PD   15-NOV-2001.
XX
PF   04-MAY-2001; 2001WO-US014508.
XX
PR   05-MAY-2000; 2000US-0202274P.
PR   17-JAN-2001; 2001US-0262321P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Raz E,  Lois AF,  Takabayashi K;
XX
DR   WPI; 2002-062244/08.
XX
PT   Modulating cell death or reducing DNA damage in eukaryotic cells, useful
PT   for reducing cell death in individual or organ, comprises contacting cell
PT   with agent modulating biological activity of DNA-dependent protein
PT   kinase.
XX
PS   Example 3; Page 33; 57pp; English.
XX
CC   The invention relates to a method for modulating cell death or reducing
CC   DNA damage in an eukaryotic cell by contacting the cell with an agent
CC   that modulates the biological activity of DNA-dependent protein kinase
CC   (DNA-PK). The invention also relates nucleic acids which modulate the
CC   immune response binding to Ku antigen, resulting in activation of DNA-PK.
CC   The method is useful for modulating cell death or reducing DNA damage in
CC   an eukaryotic cell, for treating any disorder resulting from a genotoxic
CC   insert to a cell e.g., necrosis, apoptosis. The method is also useful for
CC   treating cell death-related indications such as Alzheimer's disease,
CC   Parkinson's disease, rheumatoid arthritis, septic shock, sepsis, stroke,
CC   central nervous system inflammation, osteoporosis, degenerative liver
CC   disease, cerebellar degeneration, reperfusion injury, multiple sclerosis,
CC   amyotrophic lateral sclerosis, myocardial infarction, head injury damage,
CC   acquired immunodeficiency syndrome (AIDS), aplastic anaemia, cerebral
CC   infarction, bypass heart surgery, organ transplantation. The method is
CC   also useful for treating follicular lymphomas, carcinomas, autoimmune
CC   disorders (systemic lupus erythematosus), hormone dependent tumours,
CC   immune mediated glomerulonephritis; apoptosis and viral infections. The
CC   present sequence is methylated (5-methyl C) immunostimulatory
CC   oligodeoxynucleotide (ISS-ODN) used in the exemplification of the
CC   invention
XX
SQ   Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             92.7%;  Score 20.4;  DB 6;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 5
AAD24894
ID   AAD24894 standard; DNA; 22 BP.
XX
AC   AAD24894;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Immunostimulatory oligodeoxynucleotide (ISS-ODN) 2.
XX
KW   Cell death; DNA damage; DNA-dependent protein kinase; DNA-PK; necrosis;
KW   immune response; apoptosis; Alzheimer's disease; Parkinson's disease;
KW   rheumatoid arthritis; inflammation; osteoporosis; myocardial infarction;
KW   liver disease; reperfusion injury; carcinoma; multiple sclerosis; stroke;
KW   amyotrophic lateral sclerosis; Acquired Immune Deficiency Syndrome; AIDS;
KW   head injury damage; aplastic anaemia; tumour; organ transplantation;
KW   cerebral infarction; follicular lymphomas; systemic lupus erythematosus;
KW   viral infection; glomerulonephritis; apoptosis; autoimmune disorder;
KW   sepsis; immunostimulatory oligodeoxynucleotide; ISS-ODN; ss.
XX
OS   Unidentified.
XX
PN   WO200185910-A2.
XX
PD   15-NOV-2001.
XX
PF   04-MAY-2001; 2001WO-US014508.
XX
PR   05-MAY-2000; 2000US-0202274P.
PR   17-JAN-2001; 2001US-0262321P.
XX
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Raz E,  Lois AF,  Takabayashi K;
XX
DR   WPI; 2002-062244/08.
XX
PT   Modulating cell death or reducing DNA damage in eukaryotic cells, useful
PT   for reducing cell death in individual or organ, comprises contacting cell
PT   with agent modulating biological activity of DNA-dependent protein
PT   kinase.
XX
PS   Example 3; Page 33; 57pp; English.
XX
CC   The invention relates to a method for modulating cell death or reducing
CC   DNA damage in an eukaryotic cell by contacting the cell with an agent
CC   that modulates the biological activity of DNA-dependent protein kinase
CC   (DNA-PK). The invention also relates nucleic acids which modulate the
CC   immune response binding to Ku antigen, resulting in activation of DNA-PK.
CC   The method is useful for modulating cell death or reducing DNA damage in
CC   an eukaryotic cell, for treating any disorder resulting from a genotoxic
CC   insert to a cell e.g., necrosis, apoptosis. The method is also useful for
CC   treating cell death-related indications such as Alzheimer's disease,
CC   Parkinson's disease, rheumatoid arthritis, septic shock, sepsis, stroke,
CC   central nervous system inflammation, osteoporosis, degenerative liver
CC   disease, cerebellar degeneration, reperfusion injury, multiple sclerosis,
CC   amyotrophic lateral sclerosis, myocardial infarction, head injury damage,
CC   acquired immunodeficiency syndrome (AIDS), aplastic anaemia, cerebral
CC   infarction, bypass heart surgery, organ transplantation. The method is
CC   also useful for treating follicular lymphomas, carcinomas, autoimmune
CC   disorders (systemic lupus erythematosus), hormone dependent tumours,
CC   immune mediated glomerulonephritis; apoptosis and viral infections. The
CC   present sequence is immunostimulatory oligodeoxynucleotide (ISS-ODN) used
CC   for identifying ISS-binding protein, which is used in the exemplification
CC   of the invention
XX
SQ   Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             92.7%;  Score 20.4;  DB 6;  Length 22;
  Best Local Similarity   95.5%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22
```

```
RESULT 6
ADO55351
ID   ADO55351 standard; DNA; 22 BP.
XX
AC   ADO55351;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Immune modulatory nucleic acid (IMS) #126.
XX
KW   Immune modulatory nucleic acid; IMS; immune modulatory sequence; non CpG;
KW   self-molecule related disease; autoimmune disease; multiple sclerosis;
KW   rheumatoid arthritis; insulin-dependent diabetes mellitus;
KW   autoimmune uveitis; primary biliary cirrhosis; myasthenia gravis;
KW   Sjogren's syndrome; pemphigus vulgaris; scleroderma; pernicious anaemia;
KW   systemic lupus erythematosus; ankylosing spondylitis;
KW   autoimmune skin disease; Grave's disease; inflammatory disease;
KW   osteoarthritis; gout; pseudogout; hydroxyapatite deposition disease;
KW   asthma; bursitis; tendonitis; conjunctivitis; urethritis; cystitis;
KW   balanitis; dermatitis; spinal cord injury; peptic ulcer; hyperlipidaemia;
KW   coronary artery disease; migraine; neuroprotective; antirheumatic;
KW   antiarthritic; antidiabetic; osteopathic; antigout; antiasthmatic;
KW   antiinflammatory; ophthalmological; dermatological; vasotropic;
KW   antimigraine; vaccine; gene therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    9. .14
FT                   /*tag=  a
FT                   /note= "Core Pu-Pu-X-Y-Py-Py hexamer region"
FT   misc_feature    11. .12
FT                   /*tag=  b
FT                   /note= "GpG or non-GpG, non-CpG dinucleotide"
XX
PN   WO2004047734-A2.
XX
PD   10-JUN-2004.
XX
PF   21-NOV-2003; 2003WO-US037157.
XX
PR   21-NOV-2002; 2002US-0428643P.
XX
PA   (BAYH-) BAYHILL THERAPEUTICS INC.
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
PI   Garren H,  Ho PP,  Steinman L;
XX
DR   WPI; 2004-441065/41.
XX
PT   Pharmaceutical compositions comprising an immune modulatory nucleic acid
PT   comprising a hexamer region, useful for treating an autoimmune disease,
PT   e.g. multiple sclerosis, rheumatoid arthritis or insulin dependent
PT   diabetes mellitus.
XX
PS   Example 10; Page 68; 98pp; English.
XX
CC   The invention relates to a pharmaceutical composition for treating a
CC   disease associated with one or more self-molecules present non-
CC   physiologically in an individual (e.g., autoimmune diseases), comprising
CC   an immune modulatory nucleic acid (IMS, immune modulatory sequence)
CC   comprising a hexamer region of the formula 5'-purine-pyrimidine-[X]-[Y]-
CC   pyrimidine-pyrimidine-3', where X and Y are any naturally-occurring or
CC   synthetic nucleotides except cytosine-guanine, and a pharmaceutical
CC   carrier. The immune modulatory nucleic acid may also contain a polyG
CC   region linked 5' and/or 3' to the hexamer region. The invention also
CC   relates to a nucleic acid composition comprising a nucleic acid vector
CC   having at least one cytosine to non-cytosine substitution (preferably C
CC   to G) within a CpG motif, wherin the CpG motif is of the formula: (a) 5'-
CC   purine-pyrimidine-C-G-pyrimidine-pyrimidine-3'; or (b) 5'-purine-purine-C
CC   -G-pyrimidine-pyrimidine-3'. The immune modulatory nucleic acid sequences
CC   are useful in the treatment of disease associated with one or more self-
CC   molecules present non-physiologically in an individual, such as
CC   autoimmune diseases (e.g., multiple sclerosis, rheumatoid arthritis,
CC   insulin-dependent diabetes mellitus, autoimmune uveitis, primary biliary
CC   cirrhosis, myasthenia gravis, Sjogren's syndrome, pemphigus vulgaris,
CC   scleroderma, pernicious anaemia, systemic lupus erythematosus, ankylosing
CC   spondylitis, autoimmune skin diseases and Grave's disease); inflammatory
CC   diseases (e.g., osteoarthritis, gout, pseudogout, hydroxyapatite
CC   deposition disease, asthma, bursitis, tendonitis, conjunctivitis,
CC   urethritis, cystitis, balanitis and dermatitis); or other conditions such
CC   as spinal cord injury, peptic ulcer, hyperlipidaemia, coronary artery
CC   disease and migraine. The present sequence represents a specific example
CC   of an immune modulatory nucleic acid predicted to be useful for
CC   modulating autoimmune disease which is referred to in an example of the
CC   invention.
XX
SQ   Sequence 22 BP; 7 A; 2 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match            92.7%;  Score 20.4;  DB 12;  Length 22;
  Best Local Similarity  95.5%;  Pred. No. 3.9;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              |||||||||||||| ||||||
Db          1 TGACTGTGAACGTTAGAGATGA 22


RESULT 7
ADO55287
ID   ADO55287 standard; DNA; 22 BP.
XX
AC   ADO55287;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Immune modulatory nucleic acid (IMS) #62.
XX
KW   Immune modulatory nucleic acid; IMS; immune modulatory sequence; non CpG;
KW   self-molecule related disease; autoimmune disease; multiple sclerosis;
KW   rheumatoid arthritis; insulin-dependent diabetes mellitus;
KW   autoimmune uveitis; primary biliary cirrhosis; myasthenia gravis;
KW   Sjogren's syndrome; pemphigus vulgaris; scleroderma; pernicious anaemia;
KW   systemic lupus erythematosus; ankylosing spondylitis;
KW   autoimmune skin disease; Grave's disease; inflammatory disease;
KW   osteoarthritis; gout; pseudogout; hydroxyapatite deposition disease;
KW   asthma; bursitis; tendonitis; conjunctivitis; urethritis; cystitis;
KW   balanitis; dermatitis; spinal cord injury; peptic ulcer; hyperlipidaemia;
KW   coronary artery disease; migraine; neuroprotective; antirheumatic;
KW   antiarthritic; antidiabetic; osteopathic; antigout; antiasthmatic;
KW   antiinflammatory; ophthalmological; dermatological; vasotropic;
KW   antimigraine; vaccine; gene therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    9. .14
FT                   /*tag=  a
FT                   /note= "Core Pu-Pu-X-Y-Py-Py hexamer region"
FT   misc_feature    11. .12
FT                   /*tag=  b
FT                   /note= "GpG or non-GpG, non-CpG dinucleotide"
FT   modified_base   11
FT                   /*tag=  c
FT                   /mod_base= i
XX
PN   WO2004047734-A2.
XX
PD   10-JUN-2004.
XX
PF   21-NOV-2003; 2003WO-US037157.
XX
PR   21-NOV-2002; 2002US-0428643P.
XX
PA   (BAYH-) BAYHILL THERAPEUTICS INC.
PA   (STRD ) UNIV LELAND STANFORD JUNIOR.
```

XX
PI Garren H, Ho PP, Steinman L;
XX
DR WPI; 2004-441065/41.
XX
PT Pharmaceutical compositions comprising an immune modulatory nucleic acid
PT comprising a hexamer region, useful for treating an autoimmune disease,
PT e.g. multiple sclerosis, rheumatoid arthritis or insulin dependent
PT diabetes mellitus.
XX
PS Example 10; Page 66; 98pp; English.
XX
CC The invention relates to a pharmaceutical composition for treating a
CC disease associated with one or more self-molecules present non-
CC physiologically in an individual (e.g., autoimmune diseases), comprising
CC an immune modulatory nucleic acid (IMS, immune modulatory sequence)
CC comprising a hexamer region of the formula 5'-purine-pyrimidine-[X]-[Y]-
CC pyrimidine-pyrimidine-3', where X and Y are any naturally-occurring or
CC synthetic nucleotides except cytosine-guanine, and a pharmaceutical
CC carrier. The immune modulatory nucleic acid may also contain a polyG
CC region linked 5' and/or 3' to the hexamer region. The invention also
CC relates to a nucleic acid composition comprising a nucleic acid vector
CC having at least one cytosine to non-cytosine substitution (preferably C
CC to G) within a CpG motif, wherin the CpG motif is of the formula: (a) 5'-
CC purine-pyrimidine-C-G-pyrimidine-pyrimidine-3'; or (b) 5'-purine-purine-C
CC -G-pyrimidine-pyrimidine-3'. The immune modulatory nucleic acid sequences
CC are useful in the treatment of disease associated with one or more self-
CC molecules present non-physiologically in an individual, such as
CC autoimmune diseases (e.g., multiple sclerosis, rheumatoid arthritis,
CC insulin-dependent diabetes mellitus, autoimmune uveitis, primary biliary
CC cirrhosis, myasthenia gravis, Sjogren's syndrome, pemphigus vulgaris,
CC scleroderma, pernicious anaemia, systemic lupus erythematosus, ankylosing
CC spondylitis, autoimmune skin diseases and Grave's disease); inflammatory
CC diseases (e.g., osteoarthritis, gout, pseudogout, hydroxyapatite
CC deposition disease, asthma, bursitis, tendonitis, conjunctivitis,
CC urethritis, cystitis, balanitis and dermatitis); or other conditions such
CC as spinal cord injury, peptic ulcer, hyperlipidaemia, coronary artery
CC disease and migraine. The present sequence represents a specific example
CC of an immune modulatory nucleic acid predicted to be useful for
CC modulating autoimmune disease which is referred to in an example of the
CC invention.
XX
SQ Sequence 22 BP; 7 A; 1 C; 7 G; 6 T; 0 U; 1 Other;

Query Match 88.2%; Score 19.4; DB 12; Length 22;
Best Local Similarity 90.9%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||| |||| ||||||
Db 1 TGACTGTGAANGTTAGAGATGA 22

RESULT 8
AAV32079
ID AAV32079 standard; DNA; 22 BP.
XX
AC AAV32079;
XX
DT 09-SEP-1998 (first entry)
XX
DE Nucleotide sequence of DY1018.
XX
KW DY1018; beta-gal; ISS-PN/IMM; antigen; immune response; antibody;
KW immunisation; anaphylaxis; IgE; retinopathies; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .22
FT /*tag= a
FT /note= "phosphothioate backbone"
XX
PN WO9816247-A1.
XX
PD 23-APR-1998.
XX
PF 09-OCT-1997; 97WO-US019004.
XX
PR 11-OCT-1996; 96US-0028118P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Carson DA, Raz E, Roman M;
XX
DR WPI; 1998-261028/23.
XX
PT New immunomodulatory compositions - comprising an antigen conjugated to a
PT polynucleotide that contains an immunostimulatory sequence.
XX
PS Example 1; Page 36; 69pp; English.
XX
CC This is the nucleotide sequence of DY1018, which is conjugated to beta-
CC gal to form ISS-PN/IMM, comprising an immunomodulatory molecule (IMM),
CC which comprises an antigen conjugated to a polynucleotide (PN) that
CC contains at least one immunostimulatory nucleotide sequence (ISS). The
CC conjugate synergistically boost the magnitude of the host immune response
CC against an antigen to a level greater that the host immune response to
CC either the IMM, antigen or ISS-PN alone. These responses to ISS-PN/IMM
CC conjugates are particularly acute during the important early phase of the
CC host immune response to an antigen. The ISS-PN/IMM conjugates boost both
CC humoral (antibody) and cellular (Th1 type) immune responses of the host.
CC Thus, use of the method to boost the immune responsiveness of a host to
CC subsequent challenge by a sensitising antigen without immunisation avoids
CC the risk of Th2-mediated, immunisation-induced anaphylaxis by suppressing
CC IgE production in response to the antigen challenge. The conjugates can
CC also be used to combat pathogenic infection and to stimulate therapeutic
CC angiogenesis to treat conditions in which localised blood flow plays a
CC significant etiological role, e.g. retinopathies
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 2; Length 22;
Best Local Similarity 90.9%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||||| ||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 9
AAV80099
ID AAV80099 standard; DNA; 22 BP.
XX
AC AAV80099;
XX
DT 12-MAR-1999 (first entry)
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS Synthetic.
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US011578.
XX
PR 06-JUN-1997; 97US-0048793P.
XX

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Schwartz D, Roman M, Dina D;
XX
DR WPI; 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases.
XX
PS Claim 8; Page 29; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides
XX
SQ Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 2; Length 22;
Best Local Similarity 90.9%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||| ||||||
Db 1 TGACTGTGAACGTTCCAGATGA 22

RESULT 10
AAV80097
ID AAV80097 standard; DNA; 22 BP.
XX
AC AAV80097;
XX
DT 12-MAR-1999 (first entry)
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS Synthetic.
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US011578.
XX
PR 06-JUN-1997; 97US-0048793P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Schwartz D, Roman M, Dina D;
XX
DR WPI; 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases.
XX
PS Claim 5; Page 29; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 2; Length 22;
Best Local Similarity 90.9%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||| ||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 11
AAV80103
ID AAV80103 standard; DNA; 22 BP.
XX
AC AAV80103;
XX
DT 12-MAR-1999 (first entry)
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 11
FT /*tag= a
FT /note= "5-bromocytosine"
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US011578.
XX
PR 06-JUN-1997; 97US-0048793P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Schwartz D, Roman M, Dina D;
XX
DR WPI; 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases.
XX
PS Claim 24; Page 30; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCG,

CC GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 2; Length 22;
Best Local Similarity 90.9%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||||| ||||||
Db 1 TGACTGTGAACGTTCGAGATGA 22

RESULT 12
AAV80106
ID AAV80106 standard; DNA; 22 BP.
XX
AC AAV80106;
XX
DT 12-MAR-1999 (first entry)
XX
DE Oligo used in experiments for stimulation of cytokine production.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS Synthetic.
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US011578.
XX
PR 06-JUN-1997; 97US-0048793P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Schwartz D, Roman M, Dina D;
XX
DR WPI; 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases.
XX
PS Example 1; Page 29; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent
CC oligonucleotides that were tested for immunostimulatory activity. These
CC were used in experiments for the stimulation of cytokine production and
CC were found to lack immunostimulatory activity. The invention provides
CC specific claimed examples (AAV80096-103) of immunomodulatory sequences
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 2; Length 22;
Best Local Similarity 90.9%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGACTGTGAACGTTATAGATGA 22
||||||||||||||| ||||||
Db 1 TGACTGTGAACGTTAGCGATGA 22

RESULT 13
AAV80101
ID AAV80101 standard; DNA; 22 BP.
XX
AC AAV80101;
XX
DT 12-MAR-1999 (first entry)
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 11
FT /*tag= a
FT /note= "5-bromocytosine"
XX
PN WO9855495-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US011578.
XX
PR 06-JUN-1997; 97US-0048793P.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI Schwartz D, Roman M, Dina D;
XX
DR WPI; 1999-059898/05.
XX
PT Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases.
XX
PS Claim 22; Page 30; 63pp; English.
XX
CC The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides
XX

```
SQ   Sequence 22 BP; 6 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match            85.5%;  Score 18.8;  DB 2;  Length 22;
  Best Local Similarity  90.9%;  Pred. No. 24;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||  ||||||
Db          1 TGACTGTGAACGTTCCAGATGA 22


RESULT 14
AAV80104
ID   AAV80104 standard; DNA; 22 BP.
XX
AC   AAV80104;
XX
DT   12-MAR-1999  (first entry)
XX
DE   Oligo used in experiments for stimulation of cytokine production.
XX
KW   Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW   ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW   human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW   B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS   Synthetic.
XX
PN   WO9855495-A2.
XX
PD   10-DEC-1998.
XX
PF   05-JUN-1998;   98WO-US011578.
XX
PR   06-JUN-1997;   97US-0048793P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Schwartz D,  Roman M,  Dina D;
XX
DR   WPI; 1999-059898/05.
XX
PT   Immunostimulatory oligonucleotides regulate the immune system - and
PT   contain an immune-stimulating octanucleotide sequence; for treating
PT   cancer, allergic and infectious diseases.
XX
PS   Example 1; Page 29; 63pp; English.
XX
CC   The invention relates to immunomodulatory oligonucleotides that comprise
CC   at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC   sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC   GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC   patients needing immune regulation, such as those suffering from cancer,
CC   an allergic disease and asthma. They are also used to prevent infectious
CC   diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC   and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC   Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC   Schistosoma. The immunomodulatory sequences are used to screen for human
CC   immunostimulatory activity by incubating macrophage cells and the
CC   oligonucleotide; and determining the relative amount of Th1-biased
CC   cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent
CC   oligonucleotides that were tested for immunostimulatory activity. These
CC   were used in experiments for the stimulation of cytokine production and
CC   were found to lack immunostimulatory activity. The invention provides
CC   specific claimed examples (AAV80096-103) of immunomodulatory sequences
XX
SQ   Sequence 22 BP; 7 A; 1 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match            85.5%;  Score 18.8;  DB 2;  Length 22;
  Best Local Similarity  90.9%;  Pred. No. 24;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||  ||||  ||||||
Db          1 TGACTGTGAAGGTTAGAGATGA 22


RESULT 15
AAV80102
ID   AAV80102 standard; DNA; 22 BP.
XX
AC   AAV80102;
XX
DT   12-MAR-1999  (first entry)
XX
DE   Immunomodulatory oligo comprising an ISS sequence.
XX
KW   Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW   ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW   human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW   B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    11
FT                    /*tag=  a
FT                    /note= "5-bromocytosine"
XX
PN   WO9855495-A2.
XX
PD   10-DEC-1998.
XX
PF   05-JUN-1998;   98WO-US011578.
XX
PR   06-JUN-1997;   97US-0048793P.
XX
PA   (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI   Schwartz D,  Roman M,  Dina D;
XX
DR   WPI; 1999-059898/05.
XX
PT   Immunostimulatory oligonucleotides regulate the immune system - and
PT   contain an immune-stimulating octanucleotide sequence; for treating
PT   cancer, allergic and infectious diseases.
XX
PS   Claim 23; Page 30; 63pp; English.
XX
CC   The invention relates to immunomodulatory oligonucleotides that comprise
CC   at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC   sequences are selected from the group consisting of AACGTTCC, AACGTTCG,
CC   GACGTTCC, and GACGTTCG. The immunomodulatory sequences are used to treat
CC   patients needing immune regulation, such as those suffering from cancer,
CC   an allergic disease and asthma. They are also used to prevent infectious
CC   diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC   and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC   Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC   Schistosoma. The immunomodulatory sequences are used to screen for human
CC   immunostimulatory activity by incubating macrophage cells and the
CC   oligonucleotide; and determining the relative amount of Th1-biased
CC   cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC   specific claimed examples of such immunomodulatory oligonucleotides
XX
SQ   Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match            85.5%;  Score 18.8;  DB 2;  Length 22;
  Best Local Similarity  90.9%;  Pred. No. 24;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TGACTGTGAACGTTATAGATGA 22
              ||||||||||||||  ||||||
Db          1 TGACTGTGAACGTTCGAGATGA 22


Search completed: November  9, 2005, 18:20:01
```

Job time : 276 secs